

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,943DATE: 04/17/96
TIME: 14:57:01

INPUT SET: S9945.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING Does Not Comply
Corrected Diskette Needed

1
2
3 (1) General Information:
4
5 (i) APPLICANTS: Jeffrey M. Friedman, Yiyang Zhang, Ricardo Proenca, Margherita
6 Maffei, Jeffrey Halaas, Ketan Gajiwala, and Stephen K. Burley
7
8 (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
9 ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
10
11 (iii) NUMBER OF SEQUENCES: 99
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Klauber & Jackson
15 (B) STREET: 411 Hackensack Avenue
16 (C) CITY: Hackensack
17 (D) STATE: New Jersey
18 (E) COUNTRY: USA
19 (F) ZIP: 07601
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 08/485,943
29 (B) FILING DATE: June 7, 1995
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/438,431
34 (B) FILING DATE: May 10, 1995
35 (C) CLASSIFICATION:
36
37 (vii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: 08/347,563
39 (B) FILING DATE: November 30, 1994
40 (C) CLASSIFICATION:
41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: 08/292,345
44 (B) FILING DATE: August 17, 1994
45 (C) CLASSIFICATION:

See remarks
throughout →

RAW SEQUENCE LISTING PATENT APPLICATION US/08/485,943

DATE: 04/17/96
TIME: 14:57:07

INPUT SET: S9945.raw

46
47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Jackson Esq., David A.
49 (B) REGISTRATION NUMBER: 26,742
50 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 201 487-5800
54 (B) TELEFAX: 201 343-1684
55 (C) TELEX: 133521
56
57

ERRORED SEQUENCES FOLLOW:

429 (2) INFORMATION FOR SEQ ID NO:6:
430
431 (i) SEQUENCE CHARACTERISTICS:
432 (A) LENGTH: 167 amino acids
433 (B) TYPE: amino acid
434 (D) TOPOLOGY: linear
435
436 (ii) MOLECULE TYPE: protein
437 (A) DESCRIPTION: Human ob polypeptide lacking Gln at position 49
438
439 (vi) ORIGINAL SOURCE:
440 (A) ORGANISM: Human
441
442 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
443
444 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
445 1 5 10 15
446
447 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
448 20 25 30
449
450 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
451 35 40 45
452
453 Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
454 50 55 60
455
456 Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val
457 65 70 75 80
458
459 Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
460 85 90 95
461
462 Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
463 100 105 110

--> only 166 showed up.
IS one missing?

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,943DATE: 04/17/96
TIME: 14:57:11

INPUT SET: S9945.raw

464
465 Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp
466 115 120 125
467
468 Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val
469 130 135 140
470
471 Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu
472 145 150 155 160
473
474 Asp Leu Ser Pro Gly Cys
475 165
476
477

(2) INFORMATION FOR SEQ ID NO:7:

479
480 (i) SEQUENCE CHARACTERISTICS:
481 (A) LENGTH: 175 base pairs
482 (B) TYPE: nucleic acid
483 (C) STRANDEDNESS: double
484 (D) TOPOLOGY: linear

485
486 (ii) MOLECULE TYPE: DNA (genomic)
487 (A) DESCRIPTION: exon 2G7

488
489 (iii) HYPOTHETICAL: NO

490
491 (iv) ANTI-SENSE: NO

492
493 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

494
495 GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG TGTCGGGTCC 60

496
497 NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC TATCCAGAAA GTCCAGGATG 120

498
499 ACACCAAAAG CCTCATCAAG ACCATTGTCA NCAGGATCAC TGANATTTCA CACACG 175

500
501

(2) INFORMATION FOR SEQ ID NO:8:

502
503
504 (i) SEQUENCE CHARACTERISTICS:
505 (A) LENGTH: 18 base pairs
506 (B) TYPE: nucleic acid
507 (C) STRANDEDNESS: single
508 (D) TOPOLOGY: linear

509
510 (ii) MOLECULE TYPE: DNA (primer)
511 (A) PCR 5 primer for exon 2G7

512
513 (iii) HYPOTHETICAL: NO
514

176 showed up?
Is there an extra?
Review carefully &
edit.

Descriptions:
Insert sub heading

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,943DATE: 04/17/96
TIME: 14:57:17

INPUT SET: S9945.raw

515 (iv) ANTI-SENSE: NO

516

517 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

518

519 CCAGGGCAGG AAAATGTG

18

520

521

522 (2) INFORMATION FOR SEQ ID NO:9:

523

524 (i) SEQUENCE CHARACTERISTICS:

525 (A) LENGTH: 22 base pairs

526 (B) TYPE: nucleic acid

527 (C) STRANDEDNESS: single

528 (D) TOPOLOGY: linear

529

530 (ii) MOLECULE TYPE: DNA (primer)

--> 531 (A) PCR 3 primer for exon 2G7

532

533 (iii) HYPOTHETICAL: NO

534

535 (iv) ANTI-SENSE: YES

536

537

538 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

539

540 CATCCTGGAC TTTCTGGATA GG

22

541

542

543

623 (2) INFORMATION FOR SEQ ID NO:12:

624

625 (i) SEQUENCE CHARACTERISTICS:

--> 626 (A) LENGTH: 45 amino acids

627 (B) TYPE: amino acid

628 (D) TOPOLOGY: linear

629

630 (ii) MOLECULE TYPE: protein

631

632 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

633

634 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

635

1

5

10

15

636

637 Arg Gly Ser His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys

638

20

25

30

639

640 Glu Ala Glu Leu Ala Ala Ala Thr Ala Glu Gln

641

35

40

642

643

1231 (2) INFORMATION FOR SEQ ID NO:34:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,943DATE: 04/17/96
TIME: 14:57:22

INPUT SET: S9945.raw

1232
1233 (i) SEQUENCE CHARACTERISTICS:
1234 (A) LENGTH: 40 base pairs
1235 (B) TYPE: nucleic acid
1236 (C) STRANDEDNESS: single
1237 (D) TOPOLOGY: linear
1238
1239 (ii) MOLECULE TYPE: DNA (primer)
--> 1240 (A) PCR 5 primer for amplifying human ob cDNA sequence
1241
1242 (iii) HYPOTHETICAL: NO
1243
1244 (iv) ANTI-SENSE: NO
1245
1246
1247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
1248
1249 GTATCTCTCG AGAAAAGAGT GCCCATCCAA AAAGTCCAAG 40
1250
1251

1252 (2) INFORMATION FOR SEQ ID NO:35:
1253
1254 (i) SEQUENCE CHARACTERISTICS:
1255 (A) LENGTH: 31 base pairs
1256 (B) TYPE: nucleic acid
1257 (C) STRANDEDNESS: single
1258 (D) TOPOLOGY: linear
1259
1260 (ii) MOLECULE TYPE: DNA (primer)
--> 1261 (A) PCR 3 primer for amplifying human ob cDNA sequence
1262
1263 (iii) HYPOTHETICAL: NO
1264
1265 (iv) ANTI-SENSE: YES
1266
1267
1268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
1269
1270 GCGCGAATTC TCAGCACCCA GGGCTGAGGT C 31
1271
1272

1273 (2) INFORMATION FOR SEQ ID NO:36:
1274
1275 (i) SEQUENCE CHARACTERISTICS:
1276 (A) LENGTH: 40 base pairs
1277 (B) TYPE: nucleic acid
1278 (C) STRANDEDNESS: single
1279 (D) TOPOLOGY: linear
1280
1281 (ii) MOLECULE TYPE: DNA (primer)
--> 1282 (A) PCR 5 primer for amplifying murine ob cDNA sequence

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,943DATE: 04/17/96
TIME: 14:57:27

INPUT SET: S9945.raw

1283
1284 (iii) HYPOTHETICAL: NO
1285
1286 (iv) ANTI-SENSE: NO
1287
1288
1289 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
1290
1291 GTATCTCTCG AGAAAAGAGT GCCTATCCAG AAAGTCCAGG
1292
1293

40

1294 (2) INFORMATION FOR SEQ ID NO:37:
1295
1296 (i) SEQUENCE CHARACTERISTICS:
1297 (A) LENGTH: 31 base pairs
1298 (B) TYPE: nucleic acid
1299 (C) STRANDEDNESS: single
1300 (D) TOPOLOGY: linear
1301
1302 (ii) MOLECULE TYPE: DNA (primer)
--> 1303 (A) PCR 3 primer for amplifying murine ob cDNA sequence
1304
1305 (iii) HYPOTHETICAL: NO
1306
1307 (iv) ANTI-SENSE: YES
1308
1309
1310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
1311
1312 GCGCGAATTC TCAGCATTCA GGGCTAACAT C
1313
1314

31

2666 (2) INFORMATION FOR SEQ ID NO:95:
2667
2668 (i) SEQUENCE CHARACTERISTICS:
--> 2669 (A) LENGTH: 146 amino acids
2670 (B) TYPE: amino acid
2671 (D) TOPOLOGY: linear
2672
2673 (ii) MOLECULE TYPE: protein
2674 (A) DESCRIPTION: Recombinant murine met ob protein
2675
2676 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
2677
2678 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
2679 1 5 10 15
2680
2681 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
2682 20 25 30
2683
2684 Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro

147 shown

[illegible]

8/48,943

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR 18230) on May 1, 1990, and in the *PTO Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the *PTO Official Gazette*.

The software can be accessed/requested in the following locations:

- 1) Dial-up access to the Patent and Trademark Office Bulletin Board System.
Phone number: 703-305-8950
Cost: Free-of-charge
- 2) Dial-up access through the Internet. FTP site: ftp.uspto.gov
Login as "anonymous". Software is in directory /pub/checker
Cost: Free-of-charge
- 3) For diskette copies, telephone requests to 703-306-2600.
Cost: \$25.00

For Further Information Contact: Meredith Beckhardt at 703-308-4212.

Application No.: 08/485,943

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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